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 <150> EP 03017677.0
 10 <151> 2003-08-14
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25	Arg Tyr Phe Thr Arg Pro Val Thr Gly Ala Thr Ser Gly Ala Leu Gly	115	120 125
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50	Ser Lys Leu Arg Val Ala Trp Thr Tyr Arg Thr Gly Asp Met Ala Leu	195	200 205
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25	Ile Val Phe Leu Cys Val Ala Leu Ile Ala Thr Leu Met Ala Pro Trp	85	90 95
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35	Thr Ser Gly Ala Leu Gly Ala Ile	115	120
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45	<211> 760		
50	<212> DNA		
55	<213> Acetobacter sp. ATCC 15164		
60	<400> 21		
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70	tgaacggcgc cgaattccag ggcaccccca tcaagatcgg cgatacggtc tatatctgct	120	
75	caccccacaa catcgtctcg gccctcgacc ccgacaccgg cacggaaaag tggaagtctg	180	
80	acccccacgc ccagacgaaa gtctggcagc gctgccgcgg cgtcggctac tggcatgaca	240	
85	gcacagccac ggacgccaac gcgccctgcg cctcgcgcat cgtcctcacc acgatcgacg	300	
90	cccgccatcat caccatcgac gcccgaccgg gccaggcctg cacggatttc ggaacgaacg	360	
95	gcaacgtcaa tctcctgacc ggcctcggcc cgacagcccc cggctcctac taccgaccg	420	
100	ccgccccct cgtggcgggt gacatcgtgg tcgtcggcgg ccgcatcgcc gataacgagc	480	
105	gcacaggcga gccttcgggc gtcgtccgcg gctacgacgt ccgcaccggc gcacaggtct	540	
110	gggcctggga cgccaccaac ccgcatcgcg gcaccacacc actggccgaa ggcgagatct	600	
115	acccgcgca aacccccaac atgtggggca ccgccagcta cgacccgaaa ctcaacctcg	660	

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tcttcttccc gctcggcaac cagacccccg atttctgggg cggcgaccgc agcaaggcct 720
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 <212> PRT
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<400> 22

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15

Asp Met Ala Leu Asn Gly Ala Glu Phe Gln Gly Thr Pro Ile Lys Ile
 20 25 30

20

Gly Asp Thr Val Tyr Ile Cys Ser Pro His Asn Ile Val Ser Ala Leu
 35 40 45

25

Asp Pro Asp Thr Gly Thr Glu Lys Trp Lys Phe Asp Pro His Ala Gln
 50 55 60

30

Thr Lys Val Trp Gln Arg Cys Arg Gly Val Gly Tyr Trp His Asp Ser
 65 70 75 80

35

Thr Ala Thr Asp Ala Asn Ala Pro Cys Ala Ser Arg Ile Val Leu Thr
 85 90 95

Thr Ile Asp Ala Arg Leu Ile Thr Ile Asp Ala Arg Thr Gly Gln Ala
 100 105 110

40

Cys Thr Asp Phe Gly Thr Asn Gly Asn Val Asn Leu Leu Thr Gly Leu
 115 120 125

45

Gly Pro Thr Ala Pro Gly Ser Tyr Tyr Pro Thr Ala Ala Pro Leu Val
 130 135 140

50

Ala Gly Asp Ile Val Val Val Gly Gly Arg Ile Ala Asp Asn Glu Arg
 145 150 155 160

55

Thr Gly Glu Pro Ser Gly Val Val Arg Gly Tyr Asp Val Arg Thr Gly
 165 170 175

Ala Gln Val Trp Ala Trp Asp Ala Thr Asn Pro His Arg Gly Thr Thr
 180 185 190

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Pro Leu Ala Glu Gly Glu Ile Tyr Pro Ala Glu Thr Pro Asn Met Trp
195 200 205

5 Gly Thr Ala Ser Tyr Asp Pro Lys Leu Asn Leu Val Phe Phe Pro Leu
210 215 220

10 Gly Asn Gln Thr Pro Asp Phe Trp Gly Gly Asp Arg Ser Lys Ala Ser
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15 Asp Glu Tyr Asn Asp Ala Phe Val Ala Val Asp Ala
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20 <212> DNA
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25 <400> 23
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30 <210> 24
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35 <220>
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45 <213> Artificial

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50 <400> 25
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55 <211> 2367
<212> DNA
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<400> 26

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	gactccgacc agcccgcca tgactggccc gcctatggcc gcacagcttc cggcacgcgc	540
	tacgccagct tcacacagat caaccgcgac aatgtcagca agctccgctg cgcctggacc	600
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	ggcgatacgg totatatctg ctacccccac aacatcgtct cggccctcga ccccgacacc	720
25	ggcacggaaa agtgaagtt cgacccccac gccagacga aagtctggca gcgctgccgc	780
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	gtccgcaccg gcgcacaggc ctgggcctgg gacgccacca acccgcatcg cggcaccaca	1140
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	gccacggccc agcccatcct ctacgacatt ccggacggcc atggcggcac ccgcccggcg	1440
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<211> 788

25 <212> PRT

<213> Gluconobacter oxydans IFO 3244

<400> 27

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40 Leu Gly Gly Ser Trp Phe Tyr Thr Leu Ala Gly Ile Ala Leu Ala Ala
 35 40 45

45 Ser Ser Val Tyr Met Ile Arg Arg Asn Ile Leu Ser Thr Trp Ile Ala
 50 55 60

50 Leu Gly Leu Leu Val Ala Thr Ala Leu Trp Ser Leu Ala Glu Val Gly
 65 70 75 80

55 Thr Ser Phe Trp Pro Ser Phe Ser Arg Leu Ile Val Phe Leu Cys Val
 85 90 95

60 Ala Leu Ile Ala Thr Leu Met Ala Pro Trp Leu Ser Gly Pro Gly Arg
 100 105 110

65 Arg Tyr Phe Thr Arg Pro Val Thr Gly Ala Thr Ser Gly Ala Leu Gly
 115 120 125

5	Ala 130	Ile	Ile	Val	Ala	Phe	Leu 135	Ala	Gly	Met	Phe	Arg 140	Val	His	Pro	Thr
10	Ile 145	Ala	Pro	Gln	Asp	Thr 150	Thr	His	Pro	Gln	Glu 155	Thr	Ala	Ser	Thr	Ala 160
15	Asp	Ser	Asp	Gln	Pro 165	Gly	His	Asp	Trp	Pro 170	Ala	Tyr	Gly	Arg	Thr 175	Ala
20	Ser	Gly	Thr	Arg 180	Tyr	Ala	Ser	Phe	Thr 185	Gln	Ile	Asn	Arg	Asp 190	Asn	Val
25	Ser	Lys	Leu 195	Arg	Val	Ala	Trp	Thr 200	Tyr	Arg	Thr	Gly	Asp 205	Met	Ala	Leu
30	Asn 210	Gly	Ala	Glu	Phe	Gln	Gly 215	Thr	Pro	Ile	Lys	Ile 220	Gly	Asp	Thr	Val
35	Tyr 225	Ile	Cys	Ser	Pro	His 230	Asn	Ile	Val	Ser	Ala 235	Leu	Asp	Pro	Asp	Thr 240
40	Gly	Thr	Glu	Lys	Trp 245	Lys	Phe	Asp	Pro	His 250	Ala	Gln	Thr	Lys	Val 255	Trp
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55	Arg	Leu 290	Ile	Thr	Ile	Asp	Ala 295	Arg	Thr	Gly	Gln	Ala 300	Cys	Thr	Asp	Phe
60	Gly 305	Thr	Asn	Gly	Asn	Val 310	Asn	Leu	Leu	Thr	Gly 315	Leu	Gly	Pro	Thr	Ala 320
65	Pro	Gly	Ser	Tyr	Tyr 325	Pro	Thr	Ala	Ala	Pro 330	Leu	Val	Ala	Gly	Asp 335	Ile
70	Val	Val	Val	Gly 340	Gly	Arg	Ile	Ala	Asp 345	Asn	Glu	Arg	Thr	Gly 350	Glu	Pro
75	Ser	Gly	Val	Val	Arg	Gly	Tyr	Asp	Val	Arg	Thr	Gly	Ala	Gln	Val	Trp

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5	Ala Trp Asp Ala Thr Asn Pro His Arg Gly Thr Thr Pro Leu Ala Glu 370 375 380		
10	Gly Glu Ile Tyr Pro Ala Glu Thr Pro Asn Met Trp Gly Thr Ala Ser 385 390 395 400		
15	Tyr Asp Pro Lys Leu Asn Leu Val Phe Phe Pro Leu Gly Asn Gln Thr 405 410 415		
20	Pro Asp Phe Trp Gly Gly Asp Arg Ser Lys Ala Ser Asp Glu Tyr Asn 420 425 430		
25	Asp Ala Phe Val Ala Val Asp Ala Lys Thr Gly Asp Glu Arg Trp His 435 440 445		
30	Phe Arg Thr Ala Asn His Asp Leu Val Asp Tyr Asp Ala Thr Ala Gln 450 455 460		
35	Pro Ile Leu Tyr Asp Ile Pro Asp Gly His Gly Gly Thr Arg Pro Ala 465 470 475 480		
40	Ile Ile Ala Met Thr Lys Arg Gly Gln Ile Phe Val Leu Asp Arg Arg 485 490 495		
45	Asp Gly Thr Pro Ile Val Pro Val Glu Met Arg Lys Val Pro Gln Asp 500 505 510		
50	Gly Ala Pro Glu His Gln Tyr Leu Ala Pro Glu Gln Pro Tyr Ser Ala 515 520 525		
55	Leu Ser Ile Gly Thr Glu Arg Leu Lys Pro Ser Asp Met Trp Gly Gly 530 535 540		
	Thr Ile Phe Asp Gln Leu Leu Cys Arg Ile Gln Phe Ala Ser Tyr Arg 545 550 555 560		
	Tyr Glu Gly Glu Phe Thr Pro Val Asn Glu Lys Gln Ala Thr Ile Ile 565 570 575		
	Tyr Pro Gly Tyr Tyr Gly Gly Ile Asn Trp Gly Gly Gly Ala Val Asp 580 585 590		

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Glu Ser Thr Gly Thr Leu Leu Val Asn Asp Ile Arg Met Ala Gln Trp
 595 600 605

5 Gly Lys Phe Met Lys Gln Glu Glu Ala Arg Arg Ser Gly Phe Lys Pro
 610 615 620

10 Ser Ser Glu Gly Glu Tyr Ser Glu Gln Lys Gly Thr Pro Trp Gly Val
 625 630 635 640

Val Arg Ser Met Phe Phe Ser Pro Ala Gly Leu Pro Cys Val Lys Pro
 645 650 655

15 Pro Tyr Gly Thr Met Asn Ala Ile Asp Leu Arg Ser Gly Lys Val Lys
 660 665 670

20 Trp Ser Met Pro Leu Gly Thr Ile Gln Asp Met Pro Val His Gly Met
 675 680 685

25 Val Pro Gly Leu Ala Ile Pro Leu Gly Met Pro Thr Met Ser Gly Pro
 690 695 700

30 Leu Ala Thr His Thr Gly Leu Val Phe Phe Ser Gly Thr Leu Asp Asn
 705 710 715 720

Tyr Val Arg Ala Leu Asn Thr Asp Thr Gly Glu Val Val Trp Lys Ala
 725 730 735

35 Arg Leu Pro Val Ala Ser Gln Ala Ala Pro Met Ser Tyr Met Ser Asp
 740 745 750

40 Lys Thr Gly Lys Gln Tyr Ile Val Val Thr Ala Gly Gly Leu Thr Arg
 755 760 765

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50 Pro Ser Glu Glu
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